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## RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/763,692

TIME: 14:40:09

Input Set : N:\Crif3\RULE60\10763692.raw.txt

Output Set: N:\CRF4\08302004\J763692.raw

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1 <110> APPLICANT: Kennedy, Giulia C.
2 <120> TITLE OF INVENTION: Polynucleotides Differentially Expressed
3   in Adenocarcinomas, Polypeptides Encoded Thereby, and
4   Methods of Use Thereof
5 <130> FILE REFERENCE: 2300-1575
6 <140> CURRENT APPLICATION NUMBER: US/10/763,692
7 <141> CURRENT FILING DATE: 2004-01-22
8 <150> PRIOR APPLICATION NUMBER: US/09/626,301
9 <151> PRIOR FILING DATE: 2000-07-25
10 <150> PRIOR APPLICATION NUMBER: 60/145,612
11 <151> PRIOR FILING DATE: 1999-07-26
12 <150> PRIOR APPLICATION NUMBER: 60/148,936
13 <151> PRIOR FILING DATE: 1999-08-13
14 <160> NUMBER OF SEQ ID NOS: 19
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 4612
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo Sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (698)...(3862)
24 <400> SEQUENCE: 1
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26   ttcaaatata catatgcatg ggtcttgctg ctgcctcttt tgctgactgt aattggactt      120
27   tgaagcttcg aagttatatc ataaaaattt gtaacctttg tctgagagag agctcagcta      180
28   agcaatcact ttccactttt tttcacagga taatataaac gttttcttga aagcttggtga      240
29   acagattgga ttgaaagaag cccagctttt ccctctgga gatctacagg atttatcaaa      300
30   tcgagtcact gtcaagcaag aagagactga caggagagtg aaaaatgttt tgataacatt      360
31   gtactggctg ggaagaaaag cacaaagcaa cccgtactat aatgggtccc atcttaattt      420
32   gaaagcggtt gagaatcttt taggacaagc actgacgaag gcactcgaag actccagctt      480
33   cctgaaaaga agtggcaggg acagtggcta cggtgacatc tgggtgcctg aacgtggaga      540
34   atttcttgct cctccaaggc accataagag agaagattcc tttgaaagct tggactcttt      600
35   gggctcgagg tcattgacaa gctgctcctc tgatatcacg ttgagagggg ggcgtgaagg      660
36   ttttgaaagt gacacagatt cggaatttac attcaag atg cag gat tat aat aaa      715
37                                     Met Gln Asp Tyr Asn Lys
38                                     1           5
39   gat gat atg tcg tat cga agg att tcg gct gtt gag cca aag act gcg      763
40   Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu Pro Lys Thr Ala
41       10           15           20
42   tta ccc ttc aat cgt ttt tta ccc aac aaa agt aga cag cca toc tat      811
43   Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg Gln Pro Ser Tyr
44       25           30           35

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45	gta cca gca cct ctg aga aag aaa aag cca gac aaa cat gag gat aac	859
46	Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys His Glu Asp Asn	
47	40 45 50	
48	aga aga agt tgg gca agc ccg gtt tat aca gaa gca gat gga aca ttt	907
49	Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala Asp Gly Thr Phe	
50	55 60 65 70	
51	tca agg agt aag tcc atg agt gat gtc agc gca gaa gat gtt caa aac	955
52	Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu Asp Val Gln Asn	
53	75 80 85	
54	ttg cgt cag ctg cgt tac gag gag atg cag aaa ata aaa tca caa tta	1003
55	Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile Lys Ser Gln Leu	
56	90 95 100	
57	aaa gaa caa gat cag aaa tgg cag gat gac ctt gca aaa tgg aaa gat	1051
58	Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala Lys Trp Lys Asp	
59	105 110 115	
60	cgt cga aaa agt tac act tca gat ctg cag aag aaa gaa gag aga	1099
61	Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys Lys Lys Glu Glu Arg	
62	120 125 130	
63	gaa gaa att gaa aag cag gca ctt gag aag tct aag aga agc tct aag	1147
64	Glu Glu Ile Glu Lys Gln Ala Leu Glu Lys Ser Lys Arg Ser Ser Lys	
65	135 140 145 150	
66	acg ttt aag gaa atg ctg cag gac agg gaa tcc caa aat caa aag tct	1195
67	Thr Phe Lys Glu Met Leu Gln Asp Arg Glu Ser Gln Asn Gln Lys Ser	
68	155 160 165	
69	aca gtt ccg tca aga agg aga atg tat tct ttt gat gat gtg ctg gag	1243
70	Thr Val Pro Ser Arg Arg Arg Met Tyr Ser Phe Asp Asp Val Leu Glu	
71	170 175 180	
72	gaa gga aag cga ccc cct aca atg act gtg tca gaa gca agt tac cag	1291
73	Glu Gly Lys Arg Pro Pro Thr Met Thr Val Ser Glu Ala Ser Tyr Gln	
74	185 190 195	
75	agt gag aga gta gaa gag aag gga gca act tat cct tca gaa att ccc	1339
76	Ser Glu Arg Val Glu Glu Lys Gly Ala Thr Tyr Pro Ser Glu Ile Pro	
77	200 205 210	
78	aaa gaa gat tct acc act ttt gca aaa aga gag gac cgt gta aca act	1387
79	Lys Glu Asp Ser Thr Thr Phe Ala Lys Arg Glu Asp Arg Val Thr Thr	
80	215 220 225 230	
81	gaa att cag ctt cct tct caa agt cct gtg gaa gaa caa agc cca gcc	1435
82	Glu Ile Gln Leu Pro Ser Gln Ser Pro Val Glu Glu Gln Ser Pro Ala	
83	235 240 245	
84	tct ttg tct tct ctg cgt tca cgg agc aca caa atg gaa tca act cgt	1483
85	Ser Leu Ser Ser Leu Arg Ser Arg Ser Thr Gln Met Glu Ser Thr Arg	
86	250 255 260	
87	gtt tca gct tct ctc ccc aga agt tac cgg aaa act gat aca gtc agg	1531
88	Val Ser Ala Ser Leu Pro Arg Ser Tyr Arg Lys Thr Asp Thr Val Arg	
89	265 270 275	
90	tta aca tct gtg gtc aca cca aga ccc ttt ggc tct cag aca agg gga	1579
91	Leu Thr Ser Val Val Thr Pro Arg Pro Phe Gly Ser Gln Thr Arg Gly	
92	280 285 290	
93	atc tca tca ctc ccc aga tct tac acg atg gat gat gct tgg aag tat	1627

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94	Ile Ser Ser Leu Pro Arg Ser Tyr Thr Met Asp Asp Ala Trp Lys Tyr	
95	295 300 305 310	
96	aat gga gat gtt gaa gac att aag aga act cca aac aat gtg gtc agc	1675
97	Asn Gly Asp Val Glu Asp Ile Lys Arg Thr Pro Asn Asn Val Val Ser	
98	315 320 325	
99	acc cct gca cca agc ccg gac gca agc caa ctg gct tca agc tta tct	1723
100	Thr Pro Ala Pro Ser Pro Asp Ala Ser Gln Leu Ala Ser Ser Leu Ser	
101	330 335 340	
102	agc cag aaa gag gta gca gca aca gaa gaa gat gtg aca agg ctg ccc	1771
103	Ser Gln Lys Glu Val Ala Ala Thr Glu Glu Asp Val Thr Arg Leu Pro	
104	345 350 355	
105	tct cct aca tcc ccc ttc tca tct ctt tcc caa gac cag gct gcc act	1819
106	Ser Pro Thr Ser Pro Phe Ser Ser Leu Ser Gln Asp Gln Ala Ala Thr	
107	360 365 370	
108	tct aaa gcc aca ttg tct tcc aca tct ggt ctt gat tta atg tct gaa	1867
109	Ser Lys Ala Thr Leu Ser Ser Thr Ser Gly Leu Asp Leu Met Ser Glu	
110	375 380 385 390	
111	tct gga gaa ggg gaa atc tcc cca caa aga gaa gtc tca aga tcc cag	1915
112	Ser Gly Glu Gly Glu Ile Ser Pro Gln Arg Glu Val Ser Arg Ser Gln	
113	395 400 405	
114	gat cag ttc agt gat atg aga atc agc ata aac cag acg cct ggg aag	1963
115	Asp Gln Phe Ser Asp Met Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys	
116	410 415 420	
117	agt ctt gac ttt ggg ttt aca ata aaa tgg gat att cct ggg atc ttc	2011
118	Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe	
119	425 430 435	
120	gta gca tca gtt gaa gca ggt agc cca gca gaa ttt tct cag cta caa	2059
121	Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln	
122	440 445 450	
123	gta gat gat gaa att att gct att aac aac acc aag ttt tca tat aac	2107
124	Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn	
125	455 460 465 470	
126	gat tca aaa gag tgg gag gaa gcc atg gct aag gct caa gaa act gga	2155
127	Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys Ala Gln Glu Thr Gly	
128	475 480 485	
129	cac cta gtg atg gat gtg agg cgc tat gga aag gct ggt tca cct gaa	2203
130	His Leu Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu	
131	490 495 500	
132	aca aag tgg att gat gca act tct gga att tac aac tca gaa aaa tct	2251
133	Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser	
134	505 510 515	
135	tca aat cta tct gta aca act gat ttc tcc gaa agc ctt cag agt tct	2299
136	Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser	
137	520 525 530	
138	aat att gaa tcc aaa gaa atc aat gga att cat gat gaa agc aat gct	2347
139	Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His Asp Glu Ser Asn Ala	
140	535 540 545 550	
141	ttt gaa tca aaa gca tct gaa tcc att tct ttg aaa aac tta aaa agg	2395
142	Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu Lys Asn Leu Lys Arg	

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143		555		560		565		
144	cga tca caa ttt ttt gaa caa gga agc tct gat tcg gtg gtt cct gat							2443
145	Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp Ser Val Val Pro Asp							
146		570		575		580		
147	ctt cca gtt cca acc atc agt gcc ccg agt cgc tgg gtg tgg gat caa							2491
148	Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg Trp Val Trp Asp Gln							
149		585		590		595		
150	gag gag gag cgg aag cgg cag gag agg tgg cag aag gag cag gac cgc							2539
151	Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln Lys Glu Gln Asp Arg							
152		600		605		610		
153	cta ctg cag gaa aaa tat caa cgt gag cag gag aaa ctg agg gaa gag							2587
154	Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu Lys Leu Arg Glu Glu							
155		615		620		625		630
156	tgg caa agg gcc aaa cag gag gca gag aga gag aat tcc aag tac ttg							2635
157	Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu Asn Ser Lys Tyr Leu							
158		635		640		645		
159	gat gag gaa ctg atg gtc cta agc tca aac agc atg tct ctg acc aca							2683
160	Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser Met Ser Leu Thr Thr							
161		650		655		660		
162	cgg gag ccc tct ctt gcc acc tgg gaa gct acc tgg agt gaa ggg tcc							2731
163	Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr Trp Ser Glu Gly Ser							
164		665		670		675		
165	aag tct tca gac aga gaa gga acc cga gca gga gaa gag gag agg aga							2779
166	Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly Glu Glu Glu Arg Arg							
167		680		685		690		
168	cag cca caa gag gaa gtt gtt cat gag gac caa gga aag aag ccg cag							2827
169	Gln Pro Gln Glu Glu Val Val His Glu Asp Gln Gly Lys Lys Pro Gln							
170		695		700		705		710
171	gat cag ctt gtt att gag aga gag agg aaa tgg gag caa cag ctt cag							2875
172	Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp Glu Gln Gln Leu Gln							
173		715		720		725		
174	gaa gag caa gag caa aag cgg ctt cag gct gag gct gag gag cag aag							2923
175	Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu Ala Glu Glu Gln Lys							
176		730		735		740		
177	cgt cct gcg gag gag cag aag cgc cag gca gag ata gag cgg gaa aca							2971
178	Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu Ile Glu Arg Glu Thr							
179		745		750		755		
180	tca gtc aga ata tac cag tac agg agg cct gtt gat tcc tat gat ata							3019
181	Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val Asp Ser Tyr Asp Ile							
182		760		765		770		
183	cca aag aca gaa gaa gca tct tca ggt ttt ctt cct ggt gac agg aat							3067
184	Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu Pro Gly Asp Arg Asn							
185		775		780		785		790
186	aaa tcc aga tct act act gaa ctg gat gat tac tcc aca aat aaa aat							3115
187	Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr Ser Thr Asn Lys Asn							
188		795		800		805		
189	gga aac aat aaa tat tta gac caa att ggg aac acg acc tct tca cag							3163
190	Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn Thr Thr Ser Ser Gln							
191		810		815		820		

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194	825 830 835	
195	caa caa atc ctt cag gaa atg agg aag aga aca ccc ctt cac aat gac	3259
196	Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr Pro Leu His Asn Asp	
197	840 845 850	
198	aac agc tgg atc cga cag cgc agt gcc agt gtc aac aaa gag cct gtt	3307
199	Asn Ser Trp Ile Arg Gln Arg Ser Ala Ser Val Asn Lys Glu Pro Val	
200	855 860 865 870	
201	agt ctt cct ggg atc atg aga aga ggc gaa tct tta gat aac ctg gac	3355
202	Ser Leu Pro Gly Ile Met Arg Arg Gly Glu Ser Leu Asp Asn Leu Asp	
203	875 880 885	
204	tcc ccc cga tcc aat tct tgg aga cag cct cct tgg ctc aat cag ccc	3403
205	Ser Pro Arg Ser Asn Ser Trp Arg Gln Pro Pro Trp Leu Asn Gln Pro	
206	890 895 900	
207	aca gga ttc tat gct tct tcc tct gtg caa gac ttt agt cgc cca cca	3451
208	Thr Gly Phe Tyr Ala Ser Ser Ser Val Gln Asp Phe Ser Arg Pro Pro	
209	905 910 915	
210	cct cag ctg gtg tcc aca tca aac cgt gcc tac atg cgg aac ccc tcc	3499
211	Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr Met Arg Asn Pro Ser	
212	920 925 930	
213	tcc agc gtg ccc cca cct tca gct ggc tcc gtg aag acc tcc acc aca	3547
214	Ser Ser Val Pro Pro Pro Ser Ala Gly Ser Val Lys Thr Ser Thr Thr	
215	935 940 945 950	
216	ggg gtg gcc acc aca cag tcc ccc acc ccg aga agc cat tcc cct tca	3595
217	Gly Val Ala Thr Thr Gln Ser Pro Thr Pro Arg Ser His Ser Pro Ser	
218	955 960 965	
219	gct tca cag tca ggc tct cag ctg cgt aac agg tca gtc agt ggg aag	3643
220	Ala Ser Gln Ser Gly Ser Gln Leu Arg Asn Arg Ser Val Ser Gly Lys	
221	970 975 980	
222	cgc ata tgc tcc tac tgc aat aac att ctg ggc aaa gga gcc atg	3691
223	Arg Ile Cys Ser Tyr Cys Asn Asn Ile Leu Gly Lys Gly Ala Ala Met	
224	985 990 995	
225	atc atc gag tcc ctg ggt ctt tgt tat cat ttg cat tgt ttt aag tgt	3739
226	Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu His Cys Phe Lys Cys	
227	1000 1005 1010	
228	gtt gcc tgt gag tgt gac ctc gga ggc tct tcc tca gga gct gaa gtc	3787
229	Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser Ser Gly Ala Glu Val	
230	1015 1020 1025 1030	
231	agg atc aga aac cac caa ctg tac tgc aac gac tgc tat ctc aga ttc	3835
232	Arg Ile Arg Asn His Gln Leu Tyr Cys Asn Asp Cys Tyr Leu Arg Phe	
233	1035 1040 1045	
234	aaa tct gga cgg cca acc gcc atg tga tgtaagcctc catacgaaag	3882
235	Lys Ser Gly Arg Pro Thr Ala Met *	
236	1050	
237	cactgttgca gatagaagaa gaggtggttg ctgctcatgt agatctataa atatgtgttg	3942
238	tatgtctttt ttgctttttt ttttaaaaaa agaataactt tttttgcctc tttagattac	4002
239	atagaagcat tgtagtcttg gtagaaccag tattttttgtt gtttatttat aaggtaattg	4062
240	tgtgtgggga aaagtgcagt atttacctgt tgaattcagc atcttgagag cacaagggaa	4122

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